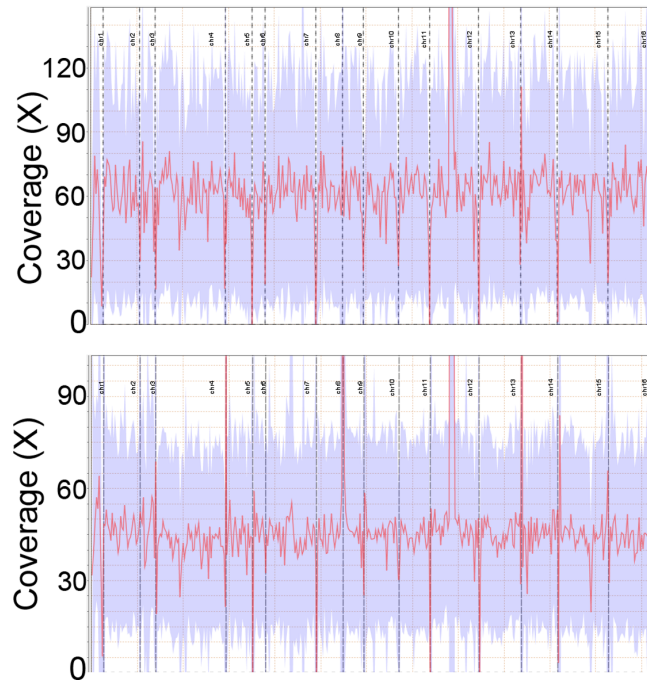


wild type
Coverage across reference



cnc1Δjhd2Δ
Coverage across reference

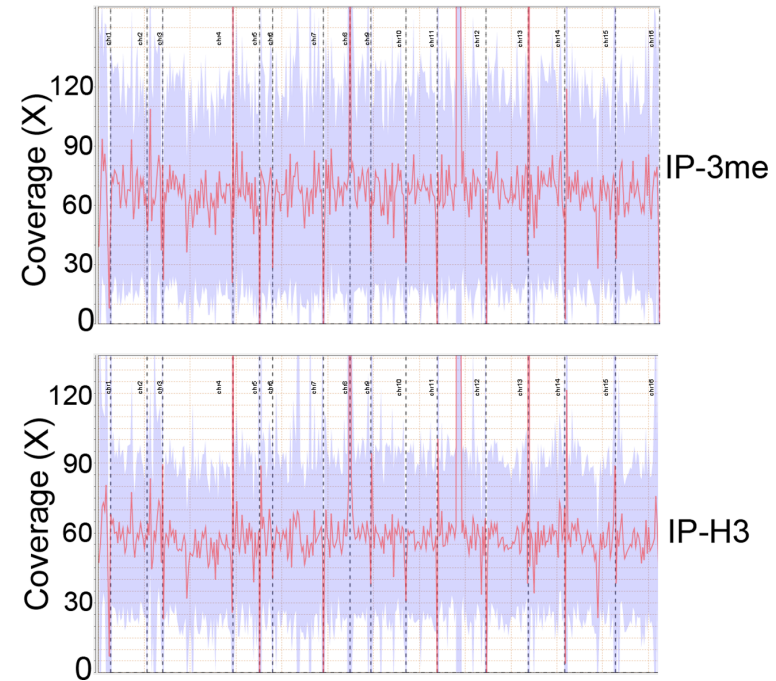


Figure S2 Representative analyses of chromosomal coverage of mapped reads by Qualimap. Fold coverage calculations performed by Qualimap for biological replicate 1, sequencing replicate 1 of ChIP-seq experiments. Red lines indicate the average fold coverage, shaded areas are the standard deviation fold coverage. Each chromosome is represented with vertical dashed lines separating them.